(FILE 'HOME' ENTERED AT 12:16:23 ON 03 NOV 2005)

FILE 'AGRICOLA, MEDLINE, CAPLUS, BIOSIS' ENTERED AT 12:16:26 ON 03 NOV 2005

L1	11349	S (NEUTRAL (1N) ENDOPEPTIDASE) OR NEP OR NEPRILYSIN
L2	900	S L1 AND (MUS OR MOUSE)
L3	323	S L2 AND (CDNA OR CLON? OR GENE)
L4	105	S L3 AND PY<1999
L5	69	DUP REM L4 (36 DUPLICATES REMOVED)
L6	0	S L5 AND 765

L6 ANSWER 10 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN
AN 1993:186782 CAPLUS
DN 118:186782
TI Murine common acute lymphoblastic leukemia antigen (CD10 neutral endopeptidase 24.11). Molecular characterization, chromosomal localization, and modeling of the active site
AU Chen, Chang Yan; Salles, Gilles; Seldin, Michael F.; Kister, Alexander E.; Reinherz, Ellis L.; Shipp, Margaret A.
CS Lab. Immunobiol., Harvard Med. Sch., Boston, MA, 02115, USA
SO Journal of Immunology (**1992**), 148(9), 2817-25
CODEN: JOIMA3; ISSN: 0022-1767
DT Journal
LA English
AB To further analyze antigen CD10/neutral endopeptidase 24.11 CD10/NEP] function in lymphoid and nonlymphoid cells using well characterized murine systems, the murine CD10/NEP homolog was isolated, its chromosomal location was determined and the enzyme active site was modeled. The murine CD10/NEP **cDNA** predicts a 750-amino acid (aa) type II integral membrane protein with 90% identity to the human CD10 sequence and 100% conservation of critical aa and functional motifs. The latter include the pentapeptide consensus sequence required for zinc binding and catalytic activity, addnl. aa associated with substrate binding, and the extracellular cysteines that participate in disulfide bonds required for enzymic activity. Like its human homolog, murine CD10/NEP has multiple alternative 5'-untranslated region sequences. The gene is localized on the proximal half of murine chromosome 3. In Northern anal., murine CD10/NEP transcripts are abundant in bone marrow stromal cells that support pre-B cell differentiation but are undetectable in representative Abelson transformed pre-B cell lines. The murine CD10/NEP active site was modeled by aligning critical conserved CD10/NEP residues with comparable residues in the active site of thermolysin, a bacterial metalloprotease with similar substrate specificity. The model predicts that the 2 enzymes have similar clefts that comprise the active site and permit zinc-dependent substrate interactions.

L6 ANSWER 8 OF 12 MEDLINE on STN DUPLICATE 4
AN 93390947 MEDLINE
DN PubMed ID: 8397369
TI NEP: a novel receptor-like tyrosine kinase expressed in proliferating neuroepithelia.
AU Zerlin M; Julius M A; Goldfarb M
CS Department of Biochemistry and Molecular Biophysics, Columbia University College of Physicians and Surgeons, New York, New York 10032.
SO Oncogene, **(1993 Oct)** 8 (10) 2731-9.
Journal code: 8711562. ISSN: 0950-9232.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199310
ED Entered STN: 19931105
Last Updated on STN: 19931105
Entered Medline: 19931018
AB We have isolated a murine **cDNA**, nep, which encodes a novel receptor-like protein tyrosine kinase. The kinase region of NEP protein bears 50% amino acid sequence identity to the neurotrophin receptors (TRKs). While the intracytoplasmic portion of NEP also contains a short kinase insert region and C-terminal tail reminiscent of the TRK proteins, the putative extracellular domain of NEP is unrelated to any known proteins. The **nep** gene is strongly expressed within proliferating neuroepithelia of **mouse** embryos, commencing at the early somite stage (embryonic day 8.0) and persisting in the proliferative ventricular zones of the brain and spinal cord, suggesting that one function of NEP kinase is to signal proliferation of neuroepithelial cells in response to an as yet unknown ligand. The nep gene is also expressed in embryonic sensory ganglia, striated muscle and epidermis, as well as in several adult tissues, including the ventricle linings and glia subpopulations in the brain.

Neutral endopeptidase modulation of septic shock.

AU Lu B; Gerard N P; Kolakowski L F Jr; Bozza M; Zurakowski D; Finco O; Carroll M C; Gerard C

CS Ina Sue Perlmutter Laboratory, Children's Hospital, Boston, Massachusetts, USA.

NC HL19170 (NHLBI)
HL51366 (NHLBI)

SO Journal of experimental medicine, **(1995 Jun 1)** 181 (6) 2271-5.
Journal code: 2985109R. ISSN: 0022-1007.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 199506

ED Entered STN: 19950707
Last Updated on STN: 19950707
Entered Medline: 19950623

AB Neutral endopeptidase (NEP; EC. 3.4.24.11) is a type 2 cell surface metalloprotease known by a variety of eponyms, including enkephalinase, common acute lymphoblastic leukemia antigen, and CD10. Identified substrates are largely neural or humoral oligopeptide agonists, and the enzyme functions to terminate signaling by degrading the ligand, analogously to acetylcholine/acetylcholinesterase. Targeted disruption of the **NEP** locus in **mice** results in enhanced lethality to endotoxin shock with a pronounced gene dosage effect. The site(s) of action appears downstream from release of tumor necrosis factor and interleukin-1 since NEP-deficient animals demonstrate increased sensitivity to these mediators as well. This unexpected finding indicates an important protective role for NEP in septic shock.

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Leu Ala Asp Asn Gln Asn Val Asn Gly Phe Ser Thr Leu Gly Glu Asn
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att gcc gac aac gga ggt gtg cga cag gca tac aag gct tac cta cgg   2368
Ile Ala Asp Asn Gly Gly Val Arg Gln Ala Tyr Lys Ala Tyr Leu Arg
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Trp Leu Ala Asp Gly Gly Lys Asp Gln Arg Leu Pro Gly Leu Asn Leu
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acc tat gcc cag ctt ttc ttc atc aac tat gcc cag gtg tgg tgt ggg   2464
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tcc tat agg ccg gag ttc gcc gtc cag tcc atc aag acg gac gtc cac   2512
Ser Tyr Arg Pro Glu Phe Ala Val Gln Ser Ile Lys Thr Asp Val His
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agt cct ctt aag tac agg gtg ctg ggc tca cta cag aac ctg cca ggc   2560
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        730                 735                 740

ttc tct gag gca ttc cac tgc cca cga ggc agc ccc atg cac ccc atg   2608
Phe Ser Glu Ala Phe His Cys Pro Arg Gly Ser Pro Met His Pro Met
    745                 750                 755

aag cga tgt cgc atc tgg tagccaaggc tgagctatgc tgcggcccac          2656
Lys Arg Cys Arg Ile Trp
760                 765

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tgaaggccac cggagccacc agccagccct ccgcgcccag cctagagtgt agccacccgc 2776

ccacacccgg gatgagtggt gccggtcctg cgccccctca ggccagtgag ggtcagcagc 2836

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 65                  70                  75                  80

Val Ile Ala Ala Ala Arg Ile Leu Glu Asn Met Asp Gln Ser Arg Asn
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Pro Cys Glu Asn Phe Tyr Gln Tyr Ala Cys Gly Gly Trp Leu Arg His
            100                 105                 110

His Val Ile Pro Glu Thr Asn Ser Arg Tyr Ser Val Phe Asp Ile Leu
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Arg Asp Glu Leu Glu Val Ile Leu Lys Gly Val Leu Glu Asp Ser Thr
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Ser Gln His Arg Pro Ala Val Glu Lys Ala Lys Thr Leu Tyr Arg Ser
145                 150                 155                 160

Cys Met Asn Gln Ser Val Ile Glu Lys Arg Asp Ser Glu Pro Leu Leu
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Ser Val Leu Lys Met Val Gly Gly Trp Pro Val Ala Met Asp Lys Trp
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Asn Glu Thr Met Gly Leu Lys Trp Glu Leu Glu Arg Gln Leu Ala Val
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225                 230                 235                 240

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His Lys Val Arg Lys Ala Tyr Leu Glu Phe Met Thr Ser Val Ala Thr
            260                 265                 270

Met Leu Arg Lys Asp Gln Asn Leu Ser Lys Glu Ser Ala Met Val Arg
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Leu Val Trp Arg Leu Val Leu Asp Arg Ile Gly Ser Leu Ser Gln Arg
385                 390                 395                 400

Phe Lys Glu Ala Arg Val Asp Tyr Arg Lys Ala Leu Tyr Gly Thr Thr
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Ser Ser Leu Thr Phe Tyr Glu Asp Leu Tyr Phe Glu Asn Gly Leu Gln
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Asn Leu Lys Asn Asn Ala Gln Arg Ser Leu Lys Lys Leu Arg Glu Lys
    530                 535                 540

Val Asp Gln Asn Leu Trp Ile Ile Gly Ala Ala Val Val Asn Ala Phe
545                 550                 555                 560

Tyr Ser Pro Asn Arg Asn Gln Ile Val Phe Pro Ala Gly Ile Leu Gln
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Pro Pro Phe Phe Ser Lys Asp Gln Pro Gln Ser Leu Asn Phe Gly Gly
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Ile Gly Met Val Ile Gly His Glu Ile Thr His Gly Phe Asp Asp Asn
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Tyr Gly Asn Phe Ser Trp Glu Leu Ala Asp Asn Gln Asn Val Asn Gly
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            660                 665                 670

Ala Tyr Lys Ala Tyr Leu Arg Trp Leu Ala Asp Gly Gly Lys Asp Gln
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Arg Leu Pro Gly Leu Asn Leu Thr Tyr Ala Gln Leu Phe Phe Ile Asn
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Tyr Ala Gln Val Trp Cys Gly Ser Tyr Arg Pro Glu Phe Ala Val Gln
705                 710                 715                 720

Ser Ile Lys Thr Asp Val His Ser Pro Leu Lys Tyr Arg Val Leu Gly
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 15                  20                  25                  30

ctg gtg gcc ttg ggt gtc ctc tac gcc gac cgc aga ggg aag cag ctg   144
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                35                  40                  45

cca cgc ctt gct agc cgg ctg tgc ttc tta cag gag gag agg acc ttt   192
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            50                  55                  60

gta aaa cga aaa ccc cga ggg atc cca gag gcc caa gag gtg agc gag   240
Val Lys Arg Lys Pro Arg Gly Ile Pro Glu Ala Gln Glu Val Ser Glu
        65                  70                  75
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